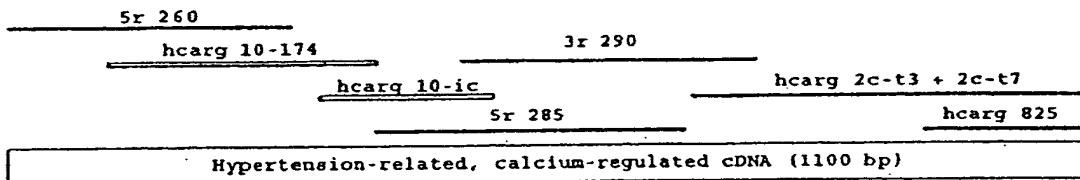


A



B

-131 GCACGAGCCACAGCCAGCTACCGCGGCTAGGTTCCCTCCAGGTGCAAGAGGGCG -80
GTAAAGGCTTGGTTGTATTGTAAATGCAACTGTGGTAGGACCTTCTCGGACTGGTCAAGAAACGGGAAGAAAGG -1
ATG TCT GCT TTG GGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC 60
Met Ser Ala Leu Gly Ala Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly
CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG ACG GCC GTG GCT CAG CTC TTG 120
Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu
AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TTG AAA CTT GTA GTC GGG GCC CTG CAT 180
Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His
GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GGT GCC AGC AAC CTG TCA GAA GAG 240
Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu
CGT CTG GCC GTC CTG CTG GCG GGC ACA CAC ACC CTG CTC CAG CAG GCT CTC CGG CTG CCC 300
Arg Leu Ala Val Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro
CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT CCT CAG 360
Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Leu Gln Glu Leu Gly Ile Pro Gln
GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCT CTT CTC GAC TCT 420
Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser
GTA GCC CAA CAG CAG GGA TCC TCG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC 480
Val Ala Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp
GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CCG AGT GTT CTC ATG CAG CTG 540
Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val Leu Met Gln Leu
AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG 600
Lys Leu Thr Asp Gly Ser Ala His Arg Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu
CGG TAC AGT GTA GCC TTG GTC CTT AAG GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC 660
Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Lys Lys Cys Glu Arg
AAA CTG CAG GAC TGA CTGAACCTGGTACTGTGGGTGCTGAAGCTGGTACAGAACACAGCCCCCCTGGTGA 734
Lys Leu Gln Asp TER
TGAGCCAACTCCATTGAGGTCTGCATGTGAGAACGTATTTAAGTGAAGAACAGCGGGACTTTCAGGTTTGTGTT 813
ATGAGTCACAGCTGGCAGGGTGGCACAGTTATAATCTCAGCCCTGGAAAGTCAGGGCTGGAGAATGGGAAGTGTGA 892
AGCTGGCCTGGCTTCATAGTGAGGCTAGTGTGAAATTAAAGAGGTAAAGCAACTATTAAAAAAAAAAAAAAA 969

FIGURE 1

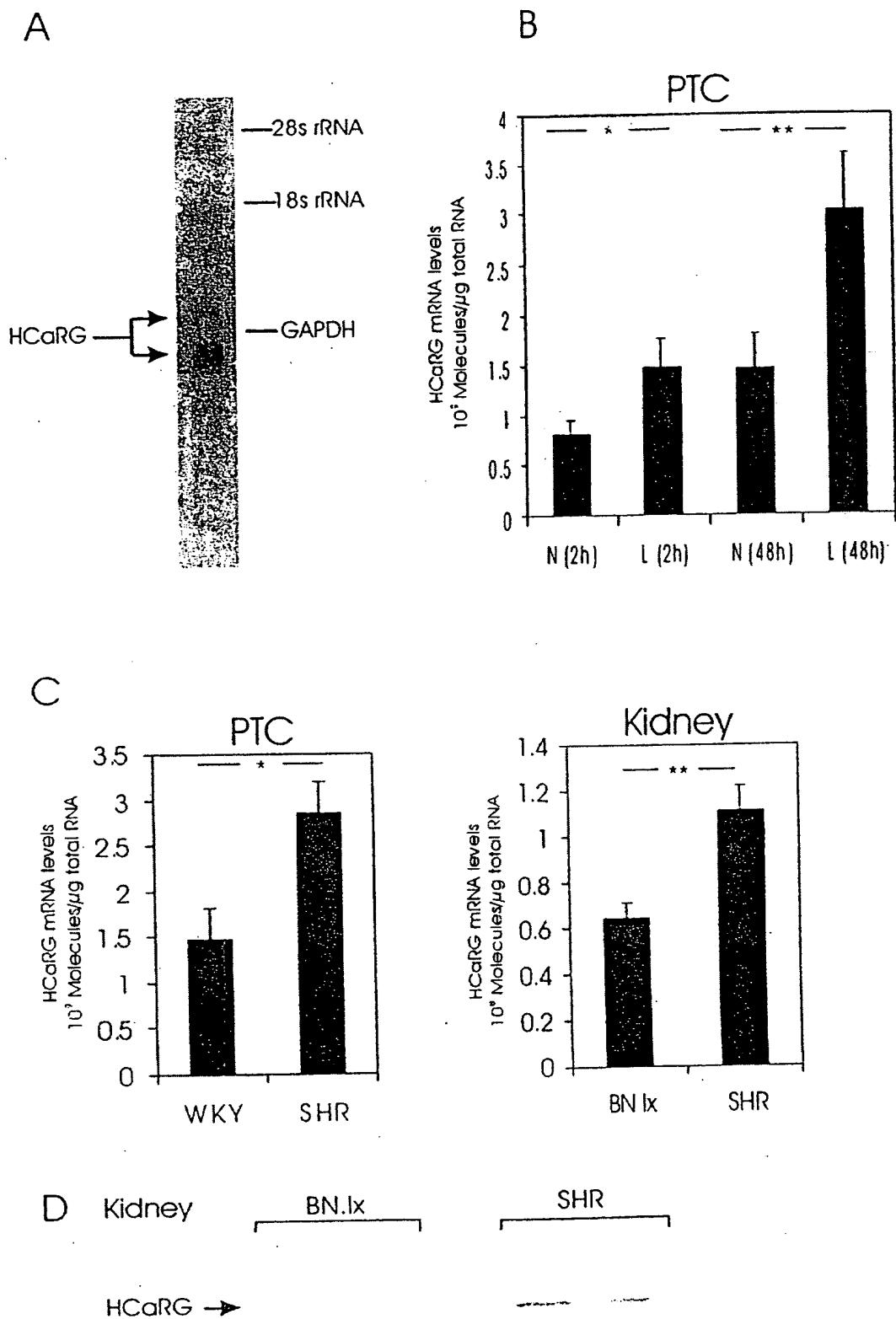


FIGURE 2

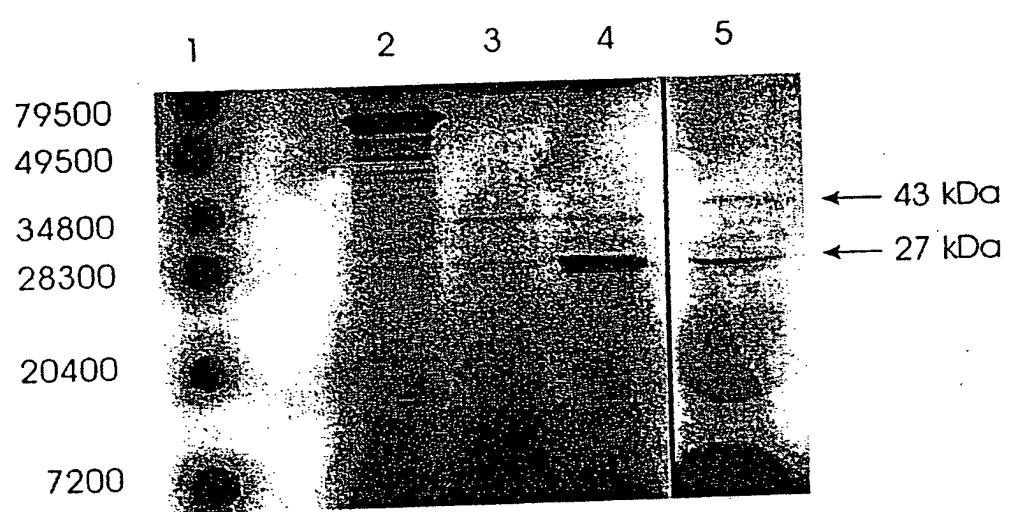


FIGURE 3

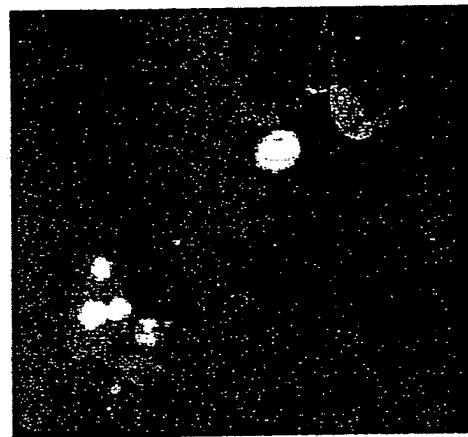
rHCArG	MSA [GAAAPY] MSA [GAAATPY] MSA [GAAATPY]	MSA [GAAATPY] MSA [GAAATPY] MSA [GAAATPY]	MSA [GAAATPY] MSA [GAAATPY] MSA [GAAATPY]	50
hHCArG			PEVIAVAPOLI [KDIIDRSTERK] PEVIAVAPOLI [KDIIDRSTERK]	50
rHCArG	ELK [LVVGA] LLK [FVVSS] PASLKPDT	ELK [LVVGA] LLK [FVVSS] PASLKPDT	ELK [LVVGA] LLK [FVVSS] PASLKPDT	100
hHCArG			GEDCREAVEQ [LGASANISEE LGASANISEE LGASANISEE]	100
rHCArG	HVS [YFRWRVD HVA [YFRWRVD	HVS [YFRWRVD HVA [YFRWRVD	HVS [YFRWRVD HVA [YFRWRVD	150
hHCArG			EFLOELCIP [DLDGLASIA DQLQELCIP [DLDGLASIA DQLQELCIP [DLDGLASIA]	150
rHCArG	RYSVALVKE RYSVALVKE	RYSVALVKE RYSVALVKE	RYSVALVKE [MLEKRCER RYSVALVKE [MLEKRCER	200
hHCArG			RYSVALVKE [MLEKRCER RYSVALVKE [MLEKRCER	200
			TDGSAPRF [EVPIIAKFOEI SDGSAPRF [EVPIIAKFOEI	224
				224

FIGURE 4

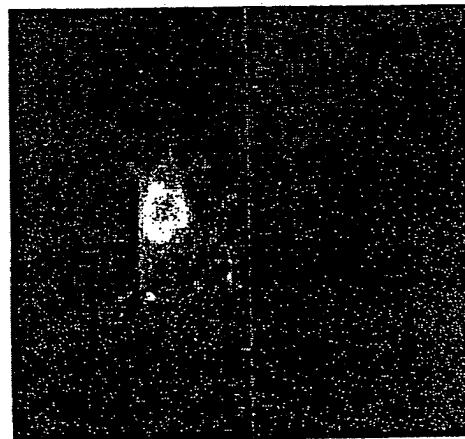
A



B



C



D

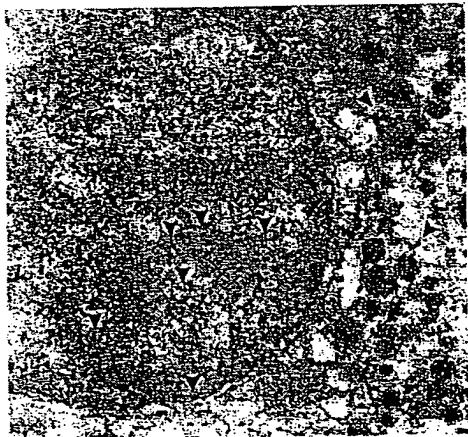
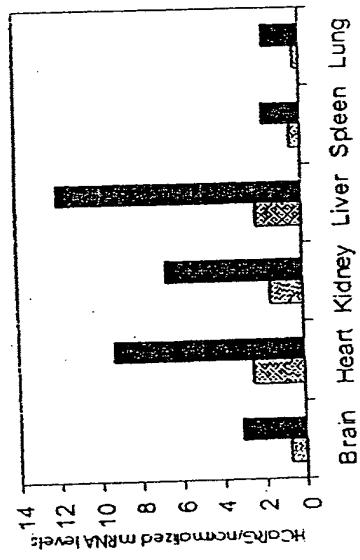
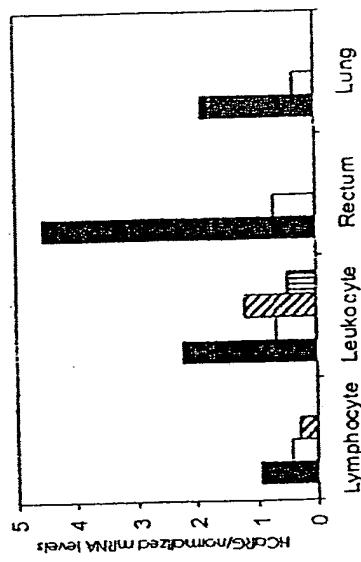


FIGURE 5

A Fetal/Adult



C Normal/Cancerous



B HEART



D Tumor/Normal

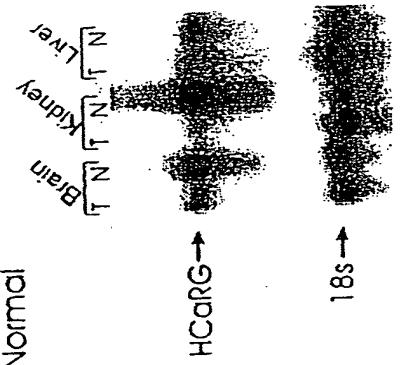


FIGURE 6

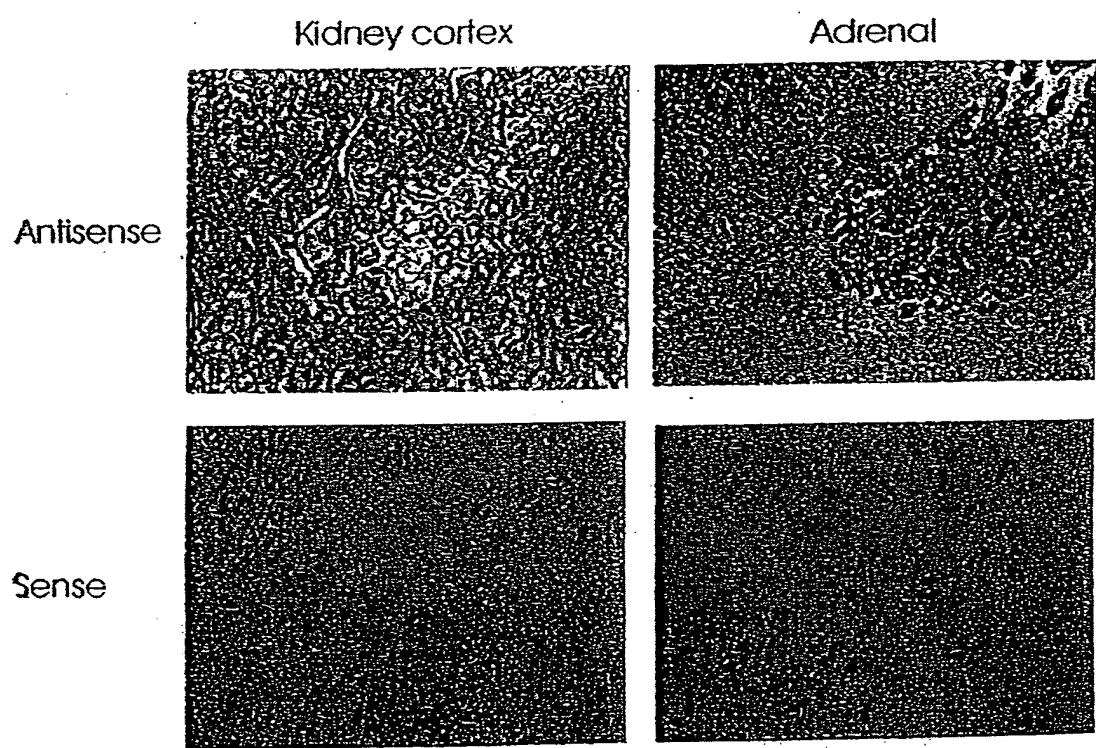
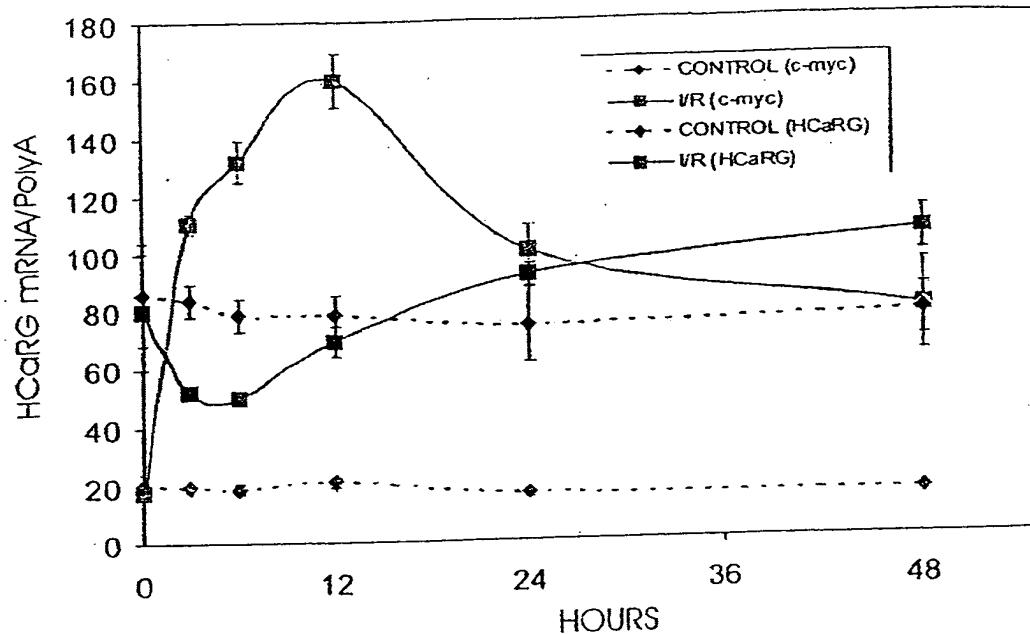
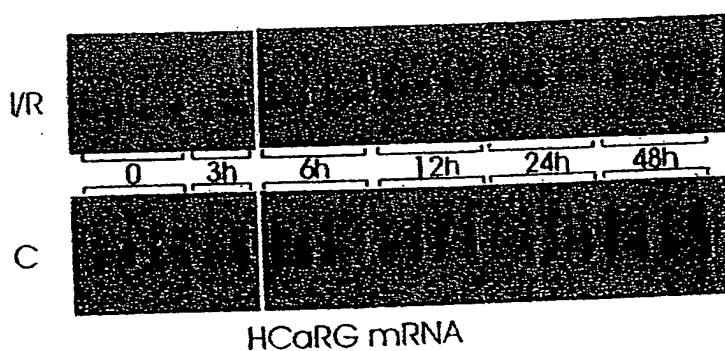


FIGURE 7

A Medulla



B Cortex



C Cortex

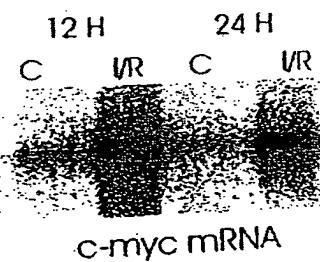
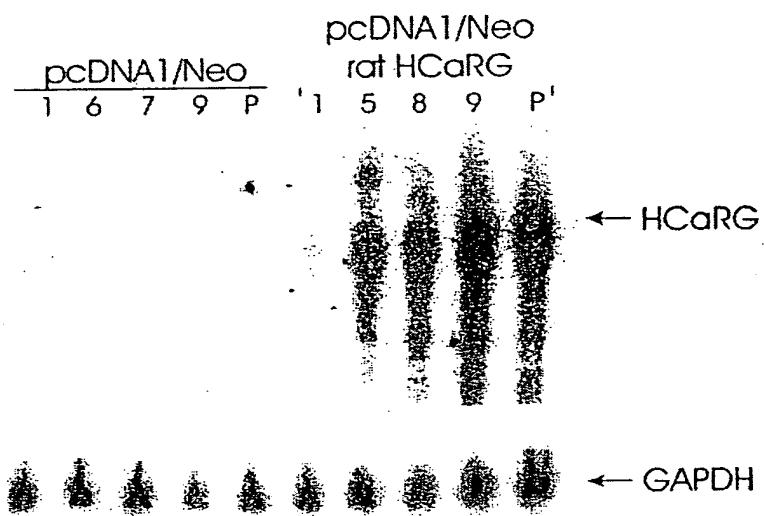


FIGURE 8

A



B

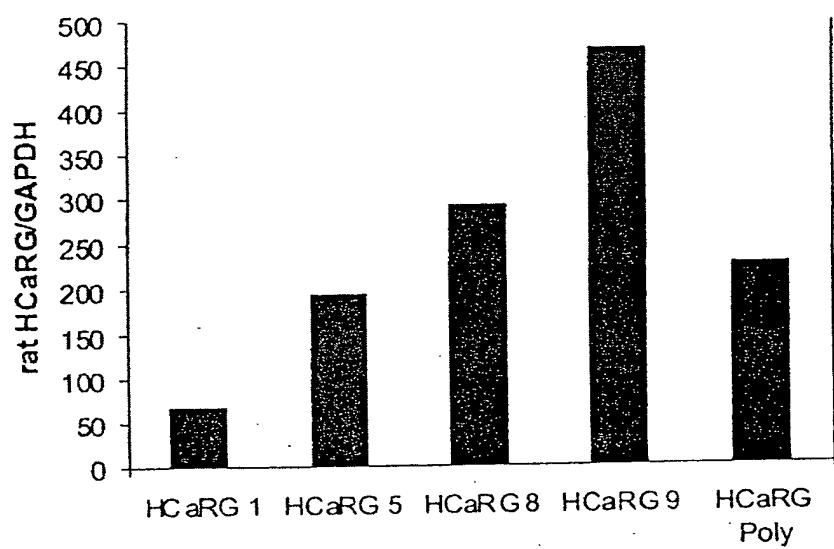
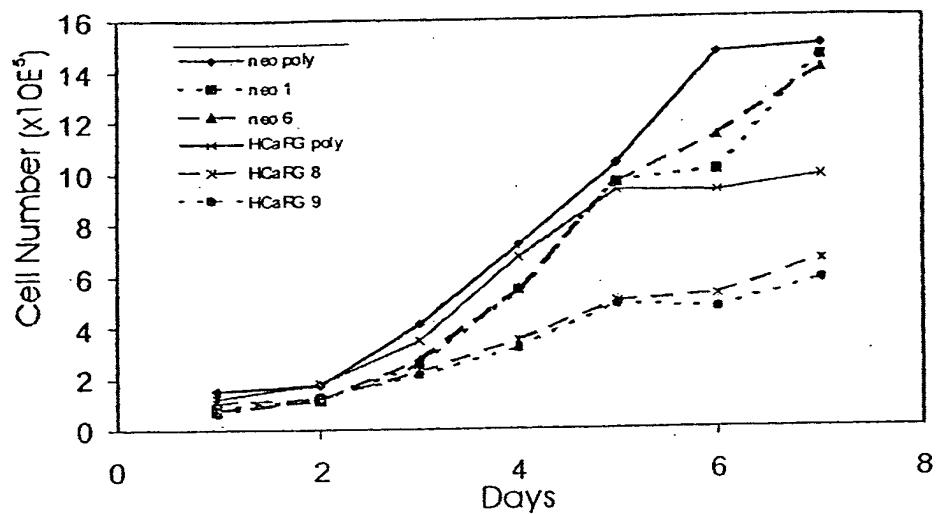


FIGURE 9

A



B

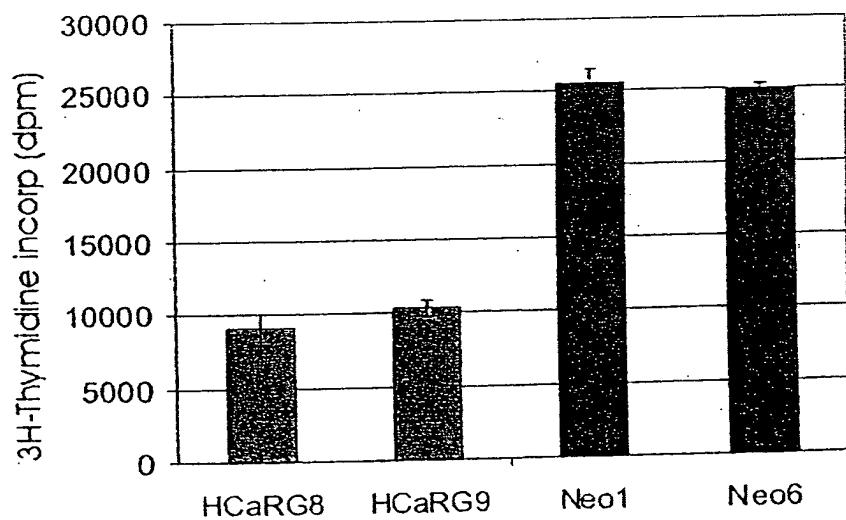


FIGURE 10

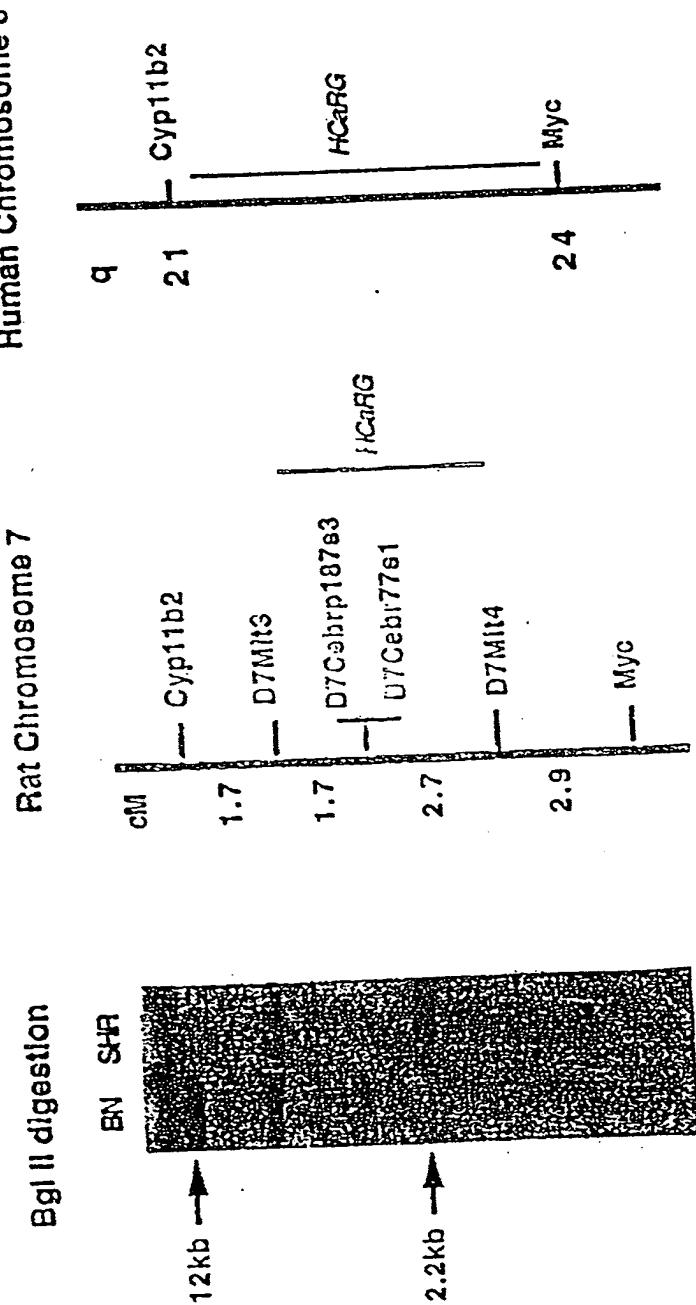


FIGURE 11